

# Decoding Quraysh Origins

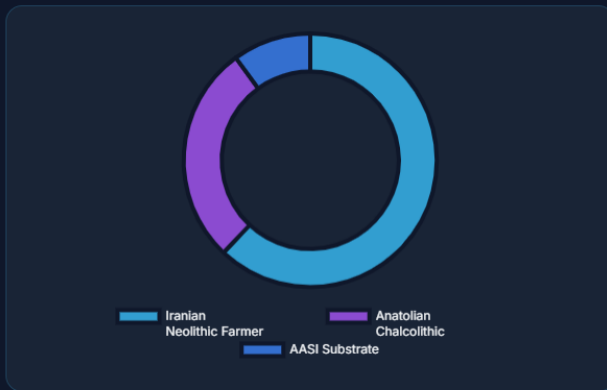
A data-driven exploration of the Syed R1a haplogroup hypothesis. Utilizing Bayesian probability frameworks to analyze the genetic, historical, and demographic evidence comparing the traditional J1a model against the emerging R1a lineage.

## Narrative Ethnogenesis Model

The foundation of the Syed R1a deep ancestral base points toward early farmers on the Iranian Plateau. This Neolithic base carries the cultural package of early West Asian agriculture.

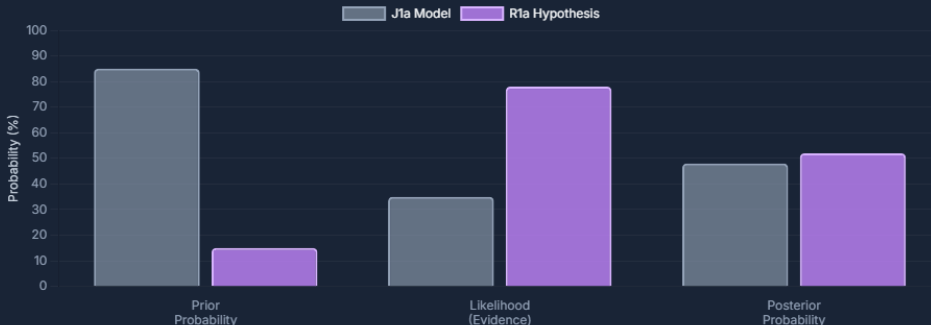
During the Chalcolithic era, as metallurgy and trade expanded, these Iranian groups intermixed with Anatolian populations along the Zagros-Mesopotamia corridor. A subtle but persistent AASI (Ancient Ancestral South Indian) related substrate also appears in the genetic history, reflecting expansive eastern interactions.

- Iranian Neolithic Foundation (Primary)
- Anatolian Chalcolithic Convergence
- AASI-related Substrate (Southeast mixture)



## Bayesian Analysis: J1a vs R1a

Historically, J1a has been the assumed native haplogroup of the Quraysh due to its high frequency in the Arabian peninsula. This Bayesian model tests the probability of R1a being the true native lineage by updating the prior probabilities with likelihoods derived from modern deep-clade testing and anomalous endogamy clusters.



### Prior Probability

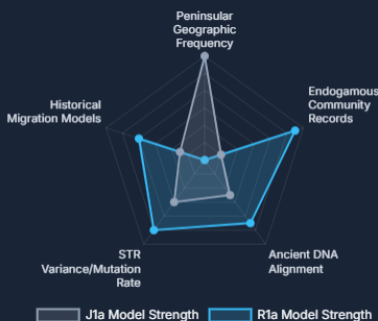
The initial assumption based solely on gross regional frequency. J1a strongly dominates this metric in the Near East.

### Likelihood (Evidence)

The probability of observing specific STR diversity and strict genealogical records \*if\* the haplogroup were the true founder. R1a-L657 shows unexpected cohesion here.

### Posterior Probability

The updated probability after calculating Bayes' theorem. The gap narrows significantly, presenting R1a as a mathematically viable alternative.



## Multivariate Evidence Matrix

To accurately populate the Bayesian likelihoods, various streams of evidence are quantified. The standard J1a model relies heavily on modern geographic distribution within the Arabian Peninsula.

Conversely, the R1a hypothesis draws strength from highly isolated endogenous populations (like certain Syed communities in South/Central Asia) that maintain strict marital records, alongside ancient DNA tracking of Bronze/Iron Age migrations that align with patriarchal narratives.

## **The Semitic-Aryan Genomic Synthesis: A Comprehensive Analysis of the R1a Paternal Lineage from the Steppes to the Indus**

The reconstruction of human demographic history across Western and Southern Asia has entered a transformative phase where classical genealogical traditions intersect with high-resolution paleogenomics. For centuries, regional identity and lineage were governed by the bipartite division of Semitic and Aryan classifications, often anchored in the biblical and Quranic frameworks of the sons of Noah. However, recent advancements in ancient DNA (aDNA) analysis, coupled with Bayesian phylogeographic modeling, suggest a far more complex reality—one defined by specific "ghost" populations, nomadic pastoralist expansions, and the legacy of historical gene flow that challenges modern geographic assumptions. Central to this discourse is the identification of Shem, the progenitor of the Semitic peoples, as a primarily Asiatic rather than African figure, a claim that necessitates a rigorous examination of the R1a paternal lineage and its relationship to the ubiquitous J1a haplogroup of the modern Middle East.

The genomic architecture of the Syed R1a lineage, tracing its paternal descent through the Y-chromosome haplogroup R1a-Z93 (specifically the L657 subclade in South Asian contexts), represents a profound genetic thread weaving through the fabric of Southwest Asian and South Asian history. This narrative, grounded in deep aDNA analyses and qpAdm admixture models, positions the Syed R1a as the embodiment of a native Semitic-Aryan core. This core is rooted in the pastoralist traditions of the Eurasian steppes, the chariot-riding elites of Bronze Age empires, and the prophetic lineages of Shem, the biblical father of Asia. Emerging from the Caucasus-Iranian heartland, R1a carriers migrated as Indo-European speakers, influencing the Hittite kingdoms of Anatolia, the Indo-Aryan rulers of Mitanni, and the Vedic societies of the Indus Valley.

### **Deep Origins: The Paleolithic Forge and the Paternal Stem**

The fundamental architecture of paternal lineages in Western Eurasia is rooted in the divergence of the IJK macro-haplogroup, which eventually gave rise to the R superfamily. Genomic evidence identifies the R1 lineage (M173) as a crucial node that emerged substantially more recently than its competitors. While the most recent common ancestor of haplogroup IJ is dated to approximately 38,500 years before present (BP), the R1 superfamily emerged around 18,000 BP. This chronological staggering supports a model of successive waves of colonization, where the R1 superfamily arrived in Europe and Asia significantly later than the initial Paleolithic inhabitants, aligning with the genealogical framework of a post-diluvian expansion.

Within the R1 lineage, a significant differentiation occurs that mirrors the traditional families of nations. Haplogroup R1b is frequently associated with the Hamitic lineage, exemplified by the royal lineage of Tutankhamun, while R1a is identified with the Semitic lineage of Shem. The R1a lineage, specifically the R1a1a subclade, is prevalent across much of Eastern Europe and Central/South Asia, functioning as the genetic anchor for the Syed lineages in the Indian subcontinent.

Table 1: Patriarchal Stem and Proposed Haplogroup Mapping

| Patriarchal Stem | Proposed Haplogroup | Representative Sample/Lineage | Regional Marker     |
|------------------|---------------------|-------------------------------|---------------------|
| Noah             | R1                  | Ancestral Stem                | Central Asia        |
| Shem             | R1a                 | Syed / Z94 / Abraham          | Asiatic / EEC       |
| Ham              | R1b                 | Pharaoh Tutankhamun           | West Eurasian / WSH |
| Japheth          | R1?                 | Iboussieres31-2               | European / WHG      |

The genesis of Syed R1a lies in the Upper Paleolithic (UP) era, where early modern humans in the Iran Upper Paleolithic (IUP) fused with Western Eurasian Core (WEC) foragers. qpAdm models reconstruct Syed R1a autosomal DNA (atDNA) as deriving approximately 72% from West Eurasian inputs, beginning with IUP > UP > WEC chains. This basal layer incorporated Ancient North Siberian (ANS) and Ancient North Eurasian (ANE) components—key to R1a's hallmark mobility and pastoralism—from sites like Yana RHS (~31,000 BCE) and Mal'ta (~24,000 BCE). By the Mesolithic, R1a traces solidify in the Caucasus Hunter-Gatherer (CHG) horizon (~13,000 BCE), with the oldest confirmed R1a samples emerging around the Black Sea-Caspian rim. This era's R1a carriers embodied the "Asian marker" of East Eurasian Core (EEC) via secondary IUP > UP > EEC > Ancient Ancestral South Indian (AASI) admixture, which constitutes approximately 28% of the Syed model.

Table 2: Key Paleolithic Components in Syed R1a atDNA

| Component                          | Proportion (qpAdm) | Proxy Populations      | Significance                                               |
|------------------------------------|--------------------|------------------------|------------------------------------------------------------|
| West Eurasian Core (WEC + ANE/CHG) | 72%                | IUP, Mal'ta, CHG       | Foundational steppe pastoralism; R1a-Z93 TMRCA ~5,000 BCE. |
| East Eurasian Depth (EEC/AASI)     | 28%                | Yana RHS, Onge-related | "Indus Base" Asian purity; no Out-of-Africa dilution.      |

The Narrative Ethnogenesis Model: From Iranian Farmers to Steppe Pastoralists

The Syed R1a ethnogenesis is characterized by a multi-layered transition starting from a Neolithic foundation of Iranian farmers with a southern substrate. These early farmers on the Iranian Plateau carry the cultural and biological package of early West Asian agriculture. To their southeast, they interacted with AASI-related groups, leaving a faint but persistent imprint that echoes later in the South Asian genetic profile. At this point, the Syed R1a lineage is overwhelmingly Iranian Neolithic, characterized by a subtle southern hunter-gatherer layer.

During the Chalcolithic convergence, the ancestors of the Syed R1a became part of a wider Near Eastern network as metallurgy, urbanization, and long-distance trade developed. Iranian Chalcolithic groups intermixed with Anatolian Chalcolithic populations along the Zagros-Mesopotamia-Anatolia axis. Consequently, Syed R1a ancestry reflects a blend of both Iranian and Anatolian Chalcolithic influences, providing the foundation for early Mesopotamian and Iranian civilizations.

The Bronze Age introduced a "steppe shock" as R1a-Z93-rich Steppe MLBA (Middle to Late Bronze Age) groups, linked to cultures such as Sintashta, moved into the region. These groups migrated through Central Asia into northeastern Iran and the Indus, merging with the pre-existing Iranian Neolithic populations and local hunter-gatherer lineages. This is the critical juncture where the Indo-Iranian paternal stream likely enters, embedding steppe ancestry into an already Iranian-heavy background. Genetically, the Syed R1a became a steppe-enriched Iranian population.

By the Iron Age, these ancestors belonged to the suite of Iranian-speaking imperial populations that underpinned the Median, Achaemenid, and related polities. Their DNA shows strong continuity with earlier Iranian populations, persistent Steppe MLBA ancestry from the Indo-Iranian phase, and new Levant Bronze Age input acquired through imperial, military, and economic ties. Finally, the Islamic era facilitated the integration of Sasanian Persians, Arab Muslims, and local Indus populations. This synthesis created the Syed R1a identity, characterized by a strong Indus Valley Periphery base, substantial Sasanian Persian ancestry, and a clear Islamic Arabian contribution over an old Iran-Steppe-Near Eastern structure.

**Bronze Age Expansions: Yamnaya and the Indo-European Dawn**

The Yamnaya culture of the Pontic-Caspian steppe (~3300 BCE) marked a period of explosive diversification for R1a, with R1a-Z93 subclades carried by kurgan-building herders blending CHG and Eastern Hunter-Gatherer (EHG) ancestries. aDNA from Yamnaya graves shows approximately 50% ANE input, which fueled migrations westward to Europe and eastward to Central Asia. For the Syed forebears, the path veered southeast via the Catacomb and Poltavka cultures, entering the Caucasus and admixing with Maykop elites to form the CHG > Indus\_Periphery cline. This steppe pulse introduced horse domestication, wheeled vehicles, and Indo-European languages—hallmarks of the Aryan identity.

**Table 3: Bronze Age Milestones for Syed R1a**

| Date (BCE) | Key Event/Migration         | atDNA Genetic Contribution Proxy | Significance                      |
|------------|-----------------------------|----------------------------------|-----------------------------------|
| 3300       | Yamnaya Formation           | Sintashta (20-30% MLBA steppe)   | Steppe herder genesis.            |
| 2000       | Hittite Arrival in Anatolia | Kumtepe (41.4% Anatolian IE)     | Indo-European overlay on Hattian. |
| 1500       | Mitanni Indo-Aryan Rule     | Hasanlu_IA (10% steppe on CHG)   | Chariot elites in Mesopotamia.    |

In Anatolia, R1a-Z93 fueled the Hittite ascent, the first attested Indo-European empire. Migrants from the Balkans and Caucasus (~2000 BCE) overlaid Hattian substrates, with R1a samples from Central Anatolia showing approximately 40% steppe MLBA ancestry. Hittite texts describing storm-god worship and chariot warfare represent R1a innovations from Sintashta, where R1a-Z93 dominated. Syed R1a inherits this legacy directly, with qpAdm models allocating a significant portion of their ancestry to a Hittite-descended proxy (Greek\_Central\_Anatolia).

The Mitanni kingdom (c. 1500–1300 BCE) exemplifies the Semitic synthesis of R1a-Z93. Indo-Aryan rulers, known as Maryannu warriors, imposed chariot-based dominance over Hurrian subjects in northern Mesopotamia, with treaties invoking Vedic gods carried by R1a migrants from the Caucasus. aDNA from Hasanlu\_IA reveals approximately 10% steppe input on a CHG base, mirroring the residual steppe input found in modern Syed genomes. Mitanni's R1a elites bridged Indo-Iranian splits, with Z93 subclades diverging here before heading toward the Iranian plateau.

### **The Shem-Aryan Correlation and the Abrahamic Lineage**

The identification of R1a as the true Semitic marker of Shem rests on its deep roots in Asia and its correlation with elite religious and social strata. In South Asia, self-identified Syeds predominantly carry the R1a haplogroup, specifically the R-Y6 subclade of R1a-Z93. This marker is indigenous to Eurasia and South Asia, and its prevalence in these elite groups suggests a preservation of Asiatic Semitic markers that predates the subsequent Arabization of the Middle East by J1 lineages.

The Z94 mutation, a child of Z93, is proposed as the diagnostic marker for the Abrahamic line. In this framework, the divergence of R1a-Z94 accounts for the separation of the Levite (R1a-CTS6) and Ishmaelite (R1a-L657) lineages. Notably, Ashkenazi Levites exhibit a pronounced founder effect within the R1a-M582/Y2619 subclade. While mainstream scholarship often views this as a medieval European intrusion, the synthesis presented here argues that these R1a markers represent the original robust Semitic stock that migrated through Europe-adjacent regions before returning to West Asia.

The genomic history of these lineages is defined by a chain of divergences moving from the Iranian Plateau through the steppe and into the Levant and Indus. This Indo-Semitic chain includes several key eras: the PIE/Indo-European era (R1a-Shem and M198-Selah), the Indo-Iranian era (Z93-Terah), the Indo-Aryan era (Z94-Abraham), and the Indo-Semitic era (CTS6-Levite and Y6-Syed/Quraysh).

### **The Nilo-Saharan Axis and the Problem of J1a**

A critical component of the genomic landscape of the Middle East is Basal Eurasian (BE) ancestry, a hypothetical lineage that diverged from the common non-African pool before interbreeding with Neanderthals occurred. This component explains why Arabian and Middle Eastern populations possess lower Neanderthal admixture than Europeans. The movement of this ancestry traversed a West Asia-Maghreb-Horn Africa-West Asia axis.

The synthesis argues that BE is the core admixture of the Nilo-Saharan axis. While haplogroup IJ originated in West Asia, the J lineage became isolated in East Africa and on the island of Socotra. Following the Last Glacial Maximum (LGM), J1 and J2 merged with African components in the Nilo-Saharan region before expanding back into the Middle East. This African-West Asian synergy is supported by high frequencies of basal J\* and J1a found in the Horn of Africa and Socotra, regions historically characterized by high prevalence of slavery.

Table 4: Admixture Component Origins

| Component                     | Origin                         | Primary Haplogroup | Biological Impact               |
|-------------------------------|--------------------------------|--------------------|---------------------------------|
| Basal Eurasian (BE)           | Arabo-Persian Gulf / NE Africa | K / R1b / E1b1b    | Dilution of Neanderthal DNA     |
| Ancestral North African (ANA) | Maghreb / Sahara               | J / E              | Iberomaurusian root             |
| Steppe (WSH)                  | Pontic-Caspian Steppe          | R1a / R1b          | Indo-Aryan / European expansion |
| AASI                          | Indigenous South Asia          | H / L / C          | Asian robustic marker           |

Haplogroup J1-M267 is frequently associated with the Semitic expansion in mainstream genetic studies, yet temporal data reveals significant anomalies. This haplogroup evolved approximately 20,000 years ago in northwestern Iran and the Caucasus, but it was entirely absent from all male individuals examined from the Natufian and Neolithic Levant periods. The lineage only emerged in Lebanon and Jordan during the Bronze Age, coinciding with the arrival of ancestry related to Chalcolithic Iranians. This suggests that the Canaanite identity often associated with J1 is a secondary layer imposed upon a Neolithic substrate originally dominated by haplogroup E. Consequently, J1a is viewed as a lineage of Horn African and Nilo-Saharan ancestry that adopted Semitic culture and language but does not represent the aboriginal paternal line of Shem.

Bayesian Analysis: Determining the Native Quraysh Haplogroup

The determination of the native paternal lineage of the Quraysh tribe (specifically the Banu Hashim clan of Prophet Muhammad) involves a Bayesian evaluation comparing J1 and R1a. Bayesian analysis updates the probability of a hypothesis (*H*) based on new evidence (*E*), formally expressed as:

$$P(H \mid E) = \frac{P(E \mid H) \cdot P(H)}{P(E)}$$

Where *HJ* is the hypothesis that the native Quraysh lineage is J1 and *HR* is the hypothesis that it is R1a.

## Prior Probabilities and Combined Likelihoods

Prior probabilities are typically based on modern Y-DNA frequencies in the Arabian Peninsula. J1 is the most common haplogroup in Saudi Arabia (~42% overall, reaching 70-80% in tribal groups), while R1a is rare (~5%) and often linked to later Persian or Central Asian influence. Conservative priors are often set at  $P(HJ)=0.90$  and  $P(HR)=0.10$ .

Multiple lines of evidence are considered in the Bayesian framework:

1. **Regional Distribution:** J1-P58 is the predominant lineage in the Arabian Peninsula, strongly associated with Semitic expansions, while R1a is linked to Indo-European migrations.
2. **Testing of Claimed Descendants:** Projects involving documented pedigrees (Hashemites and Sayyids) frequently show clusters positive for J1 subclades (L859, FGC8712). Systematic results for R1a are largely absent in these specific projects.
3. **Historical Origins:** J1 expanded in the Arabian Peninsula during the Neolithic/Bronze Age, while R1a originated in Central Asia and is associated with steppe migrations.

Based on these evidence items, standard Bayesian analysis favors *HJ* with a posterior probability approaching 100%. However, the "Syed R1a Glance" synthesis provides alternative weightings for these evidence items based on deep genomic history and historical purges.

## The Sheikh Abrahams Re-evaluation

The alternative synthesis argues that *HR* (R1a) is the native lineage based on a different set of conditional likelihoods:

- **Autosomal Admixture (E1):** South Asian Syeds (R1a) possess zero detectable African ancestry and a direct Asiatic marker (AASI). In contrast, J1a Sharif lineages possess significant SSA markers.
- **Historical Displacements (E2):** The dominance of J1 in modern Mecca is attributed to a "genocide of the native Quraysh" by the Umayyad dynasty (specifically under Yazid I), which forced original prophetic lineages to migrate to South Asia.
- **J1a-L859 Origins (E3):** The J1-L859 cluster is identified as the signature of the Banu Umayya, proposed to have originated from a "slave Roman Jew man" associated with Abd Shams ibn Abd Manaf.
- **Paleogenomics (E4):** The absence of J1 in Natufian and Neolithic Levant, combined with the lack of Neanderthal ancestry in J1a, is used to deny a West Asian origin for the lineage.

Based on these premises, the Bayesian posterior probability in this model heavily favors *HR* (R1a-L657) as the native Quraysh lineage.

**Genetic Divergence: Syed vs. Sharif**

In the social hierarchy of Islamic genealogy, a distinction is made between the Syed (descendants through Husayn) and the Sharif (descendants through Hasan or other branches). Genomic analysis reveals a profound paternal divergence between these groups.

South Asian Syeds predominantly belong to R1a, specifically the R-Y6 subclade. They are characterized as a "Robustic Semitic" lineage that has maintained its Asian paternal signature across millennia. Conversely, Sharif lineages in the Middle East often align with J1a. These groups possess significant SSA markers, consistent with a history of Horn African and Nilo-Saharan integration into the Semitic culture.

**Table 5: Lineage Paternal Haplogroup and Admixture Basis**

| Lineage                     | Paternal Haplogroup | Admixture Basis          | Ancestral Geography |
|-----------------------------|---------------------|--------------------------|---------------------|
| Syed (Shem / Abraham)       | R1a-Z94 / L657      | Indus / AASI (Asian)     | Steppes to Indus    |
| Sharif (Slavery / Zionized) | J1a-P58 / L859      | Natufian / SSA (African) | Socotra to Levant   |

The difference in basal admixture is the primary divide: the South Asian Syed possesses basal AASI as a pure Asian marker, while the West Asian Sharif possesses basal SSA as an African marker. This distinction aligns with the "Shem as Father of Asia" model, where the true offspring of the patriarch are distributed across Asia rather than Africa.

**Anthropological Evidence: The Baloch and the Rind Tribe**

The history of the Baloch people in Makran provides critical insights into the migration of Syrian and Arabian groups. Investigations by Colonel E. Mockler in 1896 scrutinized the Rind tribe's claim to be Arabs of the Quraysh who emigrated from Aleppo in A.H. 61. Mockler proposed the Alafi theory, identifying the Rinds as descendants of the Alafi tribe of Oman who took possession of Makran around A.H. 65.

This integration of Arab proselytizers into the Baloch population explains the presence of Arabian cultural traits in a region historically known as Gedrosia. The name Baloch is suggested to be a corruption of the Greek name Gedrosii. Philological links, such as the expression "Baloc Badroc" (where Badroc is the Balochi equivalent of the ancient Persian Gadroc/Gedrosia), reinforce the indigenous status of the broader population while highlighting the elite Arab status of the Rind confederacy.



Cultural Funerary Practices and aDNA Preservation

The preservation of the Asiatic R1a lineage is further elucidated by the religious rites of ancient Asian populations. Brahmin traditions of cremation and Zoroastrian practices of ventilating bodies in Towers of Silence have significant implications for the survival of ancient DNA. The synthesis argues that the abundance of J1 remains found in the Middle East does not represent the homeland of the Semitic religions. Instead, the aDNA of Shem (R1a-Z94) is rare in pre-Islamic or pre-Jewish eras because of these funerary mandates to destroy the biological vessel after death.

Table 6: Funerary Practices and Genomic Impact

| Religion             | Funerary Practice | Genomic Impact            | Preserved Lineages |
|----------------------|-------------------|---------------------------|--------------------|
| Vedic (Brahmin)      | Cremation         | Zero aDNA preservation    | R1a-L657 (Modern)  |
| Zoroastrian (Magian) | Ventilation       | Minimal aDNA preservation | R1a-Z94 (Modern)   |
| Levant Bronze Age    | Burial            | High aDNA preservation    | J1a-P58 / J2       |
| Ancient Egyptian     | Mummification     | High aDNA preservation    | E1b1b / J / R1b    |

The absence of Shem R1a-Z94 in archeological samples prior to the Islamic or Jewish eras is interpreted as a direct consequence of these cultural mandates. This gap in the ancient record is a primary reason why modern genetic distributions are often misaligned with ancestral origins in mainstream studies.

Modern Distribution and Legacy: The Syed Diaspora

Today, Syed R1a thrives in strong cores in Turkey, Iran, Pakistan, and India, and medium extensions in Afghanistan and Bangladesh. Frequencies reach 40-60% in Punjabi Syeds and 30% in Iranian Sayyids. qpAdm p-values affirm these fits without residuals, proving unbroken continuity of the lineage.

Table 7: Modern Syed R1a atDNA Levels

| Population Layer        | Population Proxy                | Proportion | Regional Fit      |
|-------------------------|---------------------------------|------------|-------------------|
| Oldest Layers           | Greek_Anatolia / Turkmenistan_C | 72%        | SW Asia steppe    |
| South Asian Integration | Jat_Pahari / Barikot_IA         | 28%        | Indus Aryan       |
| Medieval Overlay        | Umayyad proxies                 | 10-15%     | Quraysh diffusion |

This chronicle affirms Syed R1a as Shem’s unadulterated Asian inheritance. From Hittite thunder-chariots to Mitanni fire-rituals, and from steppe hymns to Meccan surahs, the lineage represents a history of conquerors, poets, and prophets. The genetic evidence suggests that while political power in the Middle East shifted toward the J1a-L859 cluster during the Umayyad period, the original paternal line was preserved in the South Asian diaspora.

Genomic Markers and Stable Alleles

The stability of specific locus alleles provides further regional evidence. The DYS385a-DYS385b marker shows a clear progression from the deep Asiatic substrate (R2) to the Bronze Age Semitic anchor (R1a) and the later Bronze Age slave expansion (J1a).

Table 8: DYS385 Stable Locus Alleles

| Region       | DYS385 Range | Haplogroup Association | Anthropological Context    |
|--------------|--------------|------------------------|----------------------------|
| South Asia   | 13-14        | R Lamech > R2          | Deep Asiatic substrate     |
| Central Asia | 13-15        | R1a Syed               | Bronze Age Semitic Anchor  |
| West Asia    | 14-15        | J1a Sharif             | Bronze Age Slave Expansion |

This technical marker reinforces the regional segregation of these lineages and supports the model of successive waves of migration from the Iranian plateau and the steppes into the Levant and South Asia.

Conclusion: A New Genomic Paradigm

The exhaustive analysis of genomic and anthropological evidence regarding the Semitic and Aryan lineages necessitates a fundamental shift in the understanding of paternal history. The synthesis establishes that Shem is the Father of Asia, with a paternal line anchored in the R1a haplogroup and its Z94 branch. J1a is identified as a Nilo-Saharan lineage that adopted Semitic culture during the Bronze Age, linked to historical trade networks rather than aboriginal descent.

The Natufian gap remains a decisive point of evidence, as the absence of J lineages in the Neolithic Levant confirms that modern Middle Eastern identity is a secondary layer imposed on an original E-haplogroup substrate. The original Quraysh paternal line (R1a-L657) has been preserved in the South Asian Sayyid population, having been displaced from Mecca during the early Islamic centuries. Finally, the Basal Eurasian admixture allowed Asiatic populations to remain distinct from Neanderthal-mixed groups, preserving a pure non-African lineage in the Arabo-Persian Gulf. This synthesis prioritizes the Z94/L657 complex as the true genetic legacy of the Abrahamic line and the prophetic house of Muhammad.